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Reference Abstract

Apidaecin multipeptide precursor structure: a putative mechanism for amplification of the insect antibacterial response.

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Apidaecins are the most prominent components of the honeybee humoral defense against microbial invasion. Our analysis of cDNA clones indicated that up to 12 of these short peptides (2 kDa) can be generated by processing of single precursor proteins; different isoforms are hereby linked in one promolecule. Assembly of the multipeptide precursors and the putative three-step maturation are strongly reminiscent of yeast alpha-mating factor. Bioactive apidaecins are flanked by the two 'processing' sequences, EAEPEAEP (or variants) and RR; joined together, they form a single unit that is repeated numerous times. The number of such repeats is variable and was reflected in the observed diversity of transcript lengths. Each such transcript is likely to be encoded by a different gene, forming a tight gene cluster. While transcriptional activation upon bacterial challenge is not exceptionally fast, the multigene and multipeptide precursor nature of the apidaecin genetic information allows for amplification of the response, resulting in a real overproduction of peptide antibiotic. Enhanced efficiency of the 'immune' response to bacterial infection through such a mechanism is, to our knowledge, unique among insects.

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